algorithm is adapted to give the largest match between sequences tested, over the entire length of the second reference polynucleotide or the complement thereof.

48. (Amended) The isolated polynucleotide of claim [47] 1, comprising (a) a first polynucleotide having at least 95% identity to the first reference polynucleotide, or (b) the complement of the entire length of such first polynucleotide.

REMARKS

This Amendment is responsive to the Official Action (Paper No. 13) mailed on August 4, 1998, which Official Action was made final. In the Office Action, the examiner noted that the specification has been amended to recite the priority information after the first paragraph; objected to certain alleged informalities in the specification; objected to claims 1, 4, 5, 7, 29 and 48; rejected claims 1-5, 7-11, 25-45, 47 and 48 under 35 U.S.C. § 112, first paragraph; rejected claims 1-3, 7-11, 25, 27, 28 and 31-48 under 35 U.S.C. § 112, second paragraph; and stated that claims 4 and 5 would be allowable if rewritten in independent form.

Claims 1-5, 7-11 and 25-48 were pending in the application. Claims 26 and 29-30 have been canceled without prejudice or disclaimer of the subject matter therein. Claims 1-5, 7, 9, 25, 27-28, 34-35, 39-41 and 46-48 have been amended. In view of the foregoing amendments and the following response, Applicant believes that claims 1-5, 7-11, 25, 27-28 and 31-48, as amended, are in condition for allowance. Reconsideration and allowance are respectfully requested.

Claims

Claims 26 and 29-30 have been canceled, without prejudice or disclaimer of the subject matter contained therein. Claims 1-5, 7, 9, 25, 27-28, 34-35, 39-41 and 46-48 have been amended. No new matter is added.

Any amendments made herein to the claims were made solely to expedite or otherwise facilitate prosecution and were not made, nor should they be construed to have been made, to overcome any issue of unpatentability of the claims as they existed prior to such amendments.

It is not believed that entry of this Amendment will require payment of any additional claim fees. Notwithstanding, the Commissioner is hereby authorized to charge any fees under 37 CFR 1.16 and 1.17 that may be required by entry of this Amendment to Deposit Account No. 50-0258.

Support

Support for the amendments is either apparent, or is as described in the text below. The recitals of sequence relatedness, such as the recital "wherein said identity is determined using an algorithm consisting of BLASTN, where the algorithm is adapted to give the largest match between sequences tested, over the entire length of the reference sequence," finds support at page 8, lines 9-31. The recitals of sequence relatedness, such as the recital "identical to the reference sequence, except that over the entire length of the reference polynucleotide there are up to ten amino acid substitutions, additions and deletions," finds support at page 16, lines 26-33. The recital of the definition of stringent hybridization conditions in claims 46 and 47, namely "wherein stringent hybridization conditions means hybridization will occur only if there is at least 95% identity between the sequences", finds support at page 17, lines 15-19. No new matter is added by the foregoing amendments to the claims.

Specification

The Examiner objected to the specification as containing certain asserted informalities. The specification has been amended as suggested by the Examiner. Withdrawal of this objection to the specification is requested.

Claim Objections

The Examiner objected to claims 1, 5, 7, 29 and 30 for certain asserted informalities. These claims have been amended as suggested by the Examiner. Withdrawal of this objection to the claims is requested.

The Examiner also objected to the form of claim 48. Claim 48 has been amended to depend from claim 1 rather than claim 47. As amended claim 48 is in proper dependent form. Reconsideration and withdrawal of this objection are respectfully requested.

Rejections Under 35 U.S.C. §112, First Paragraph

Claims 1-5, 7-11, 25-45, 47 and 48 stand rejected under 35 U.S.C. § 112, first paragraph. Specifically, the Examiner's maintains this rejection asserting that

> [t]here is no clear support in the specification as originally filed for calculating sequence similarity using the "default parameters" of any publicly available algorithm, including those specifically recited in claims 1-5, 7-11, 25, 27-45, 47 and 48 or using the algebraic formula recited in claim 26. Thus, there is no indication that such limitations were contemplated at the time the invention was made, and the limitations are new matter.

In addition, the Examiner maintained the previous rejection to claims 1-3 and 7-11 under 35 U.S.C. § 112, first paragraph, and extends that rejection to claims 25, 27, 28, 31-45, 47 and 48. Applicant respectfully traverses. For the reasons stated in the preceding amendment filed on June 29, 1998, Applicant asserts that the Examiner's grounds for this rejection are not well founded. Notwithstanding, solely to facilitate prosecution, and in no way acquiescing to the Examiner's asserted basis for this rejection, Applicant has elected to present the invention in different terms. Particularly, claims 1 and 7 have been amended to recite 90% identity and to recite that identity is determined using an algorithm consisting of BLASTN where the algorithm is adapted to give the largest match between sequences tested, over the entire length of the reference polynucleotide sequence. Applicant further asserts that claims 25, 34 and 39-40 have been amended to recite that the isolated polynucleotide is a reference polynucleotide or is "identical to the reference polynucleotide, except that over the entire length of the reference polynucleotide there are up to ten amino acid substitutions, additions and deletions." Applicant asserts that claims 1, 7, 25, 34, 39-40 and 46, as amended, are surely enabled by the specification as originally filed. In view of Applicant's election to present the invention in different terms, it is believed that the alleged

grounds for this rejection have been obviated. Reconsideration and withdrawal of the rejection to claims 1-5, 7-11 and 47-48 under 35 U.S.C. § 112, first paragraph, are respectfully requested.

Rejections Under 35 U.S.C. § 112, Second Paragraph

Claims 1-3, 7-11, 25, 27, 28 and 31-48 stand rejected under 35 U.S.C. § 112, second paragraph.

Particularly, the Examiner rejected claims 1, 7, 25, 34, 39 and 40 and claims dependent thereon asserting that they are indefinite because they recite "algorithm with default parameters . . . FASTA". Without conceding the validity of the rejection, Applicant respectfully submits that because the form of claims 1, 7, 25, 34, 39 and 40 has changed, the asserted basis for this rejection no longer applies.

The Examiner rejected claims 2, 3, 27 and 28 asserting that "'The polynucleotide' lacks proper antecedent basis in the claim since the base claims recite 'reference polynucleotide' as well as 'isolated polynucleotide'". Without conceding the validity of the rejection, Applicant submits that because the form of claims 2-4 and 27-28 has changed to insert the term –isolated-- between "The" and "polynucleotide", the asserted basis for this rejection no longer applies.

The Examiner rejected claims 35 and 41 asserting that there is insufficient antecedent basis for the term "the DNA". Claims 35 and 41 have been amended. As amended claims 35 and 41 are definite. Reconsideration and withdrawal of this rejection are respectfully requested.

The Examiner rejected claims 46-48 asserting that the term "hybridizes under stringent conditions" is indefinite. Without conceding the validity of this rejection, Applicant submits that because the form of claims 46-47 has changed to recite "wherein stringent hybridization conditions means that hybridization will occur only if there is at least 95% identity between the sequences, where identity is determined using an algorithm consisting of BLASTN where the algorithm is adapted to give the largest match between sequences tested, over the entire length of the polynucleotide sequence or fragment thereof", the asserted basis for this rejection no longer applies. Reconsideration and withdrawal of this rejection are respectfully requested.

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In view of the foregoing discussion and amendments to the claims, reconsideration and withdrawal of the rejections to the claims under 35 U.S.C. § 112, second paragraph, are respectfully requested.

Allowable Subject Matter

The Examiner noted that claim 4 and 5 would be allowable if rewritten in independent form.

Closing Remarks

Applicant thanks the Examiner for the Office Action and believes this response to be a full and complete response to such Office Action. Accordingly, favorable reexamination, reconsideration in view of this response and allowance of the pending claims are earnestly solicited.

Respectfully submitted,

Date: November 3, 1998

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APPENDIX I

Clean Set of Claim Following Entry of Amendment Filed November 3, 1998

1. (Twice Amended) An isolated polynucleotide comprising a member selected from the group consisting of:

(a) a first polynucleotide having at least a 90% identity to a reference polynucleotide sequence consisting of a sequence encoding a polypeptide comprising amino acids 1 to 256 of SEQ ID NO:2, wherein said identity is determined using an algorithm consisting of BLASTN, where the algorithm is adapted to give the largest match between sequences tested, over the entire length of the reference polynucleotide sequence; and of

(b) a polynucleotide which is the complement of the entire length such first polynucleotide of (a).

2. (Amended) The isolated polynucleotide of Claim 1 wherein the isolated polynucleotide is DNA.

3. (Amended) The isolated polynucleotide of Claim 1 wherein the isolated polynucleotide is RNA.

4. (Twice Amended) The isolated polynucleotide of Claim 2 comprising nucleotides 1 to 771 set forth in SEQ ID NO:1.

5. (Twice Amended) The isolated polynucleotide of Claim 2 comprising a polynucleotide encoding the amino acid sequence set forth in SEQ ID NO:2.

7. (Twice Amended) An isolated polynucleotide comprising a member selected from the group consisting of:

(a) a first polynucleotide having at least a 90% identity to a reference polynucleotide which consisting of a sequence encoding the same mature polypeptide expressed by the FabI gene contained

in *Staphylococcus aureus* WCUH 29 contained in NCIMB Deposit No.40771, wherein identity is determined using an algorithm consisting of BLASTN, where the algorithm is adapted to give the largest match between sequences tested, over the entire length of the reference polynucleotide; and of

(b) a polynucleotide which is the complement of the entire length such first polynucleotide of (a).

8. A vector comprising the DNA of Claim 2.

9. A cultured host cell comprising the vector of Claim 8.

10. A process for producing a polypeptide comprising the step of culturing the host cell of Claim 9 under conditions effective to express a Fab I polypeptide encoded by the first polynucleotide.

11. A process for producing a cell which expresses a polypeptide comprising transforming or transfecting the cell with the vector of Claim 8 such that the cell expresses a Fab I polypeptide encoded by the the first polynucleotide.

25. (Amended) An isolated polynucleotide comprising (a) a first polynucleotide, wherein the first polynucleotide is (i) a reference polynucleotide consisting of a sequence encoding a polypeptide comprising the amino acids of SEQ ID NO:2, or (ii) identical to the reference polynucleotide, except that over the entire length of the reference polynucleotide there are up to ten amino acid substitutions, additions and deletions; or (b) the complement of the entire length of such first polynucleotide.

27. (Amended) The isolated polynucleotide of Claim 25 wherein the isolated polynucleotide is DNA.

28. (Amended) The isolated polynucleotide of Claim 25 wherein the isolated polynucleotide is RNA.

31. The isolated polynucleotide of claim 25, wherein the first polynucleotide sequence encodes an enoyl-ACP reductase polypeptide.

32. The isolated polynucleotide of claim 25 comprising the first polynucleotide.

33. The isolated polynucleotide of claim 25 comprising the complement of the first polynucleotide.

34. (Amended) An isolated polynucleotide comprising (a) a first polynucleotide, wherein the first polynucleotide is (i) a reference polynucleotide sequence consisting of a sequence encoding the same mature polypeptide expressed by the Fab I gene contained in NCIMB Deposit No. 40771, or (ii) identical to the reference polynucleotide, except that over the entire length of the reference polynucleotide there are up to ten amino acid substitutions, additions and deletions; or (b) the complement of the entire length of such first polynucleotide.

35. (Amended) A vector comprising the isolated polynucleotide of Claim 34, wherein the isolated polynucleotide is DNA.

36. A cultured host cell comprising the vector of Claim 35.

37. A process for producing a polypeptide comprising: expressing from the host cell of Claim 36 a polypeptide encoded by said DNA.

38. A process for producing a cell which expresses a polypeptide comprising transforming or transfecting the cell with the vector of Claim 35 such that the cell expresses the polypeptide encoded by the DNA contained in the vector.

39. (Amended) An isolated polynucleotide comprising (a) a first polynucleotide, wherein the first polynucleotide is (i) a reference polynucleotide consisting of a sequence encoding a polypeptide comprising amino acids of SEQ ID NO:2, or (ii) identical to the reference polynucleotide, except that over the entire length of the reference polynucleotide there are up to five amino acid substitutions, additions and deletions; or (b) the complement of the entire length of such first polynucleotide.

40. (Amended) An isolated polynucleotide comprising (a) a first polynucleotide, wherein the first polynucleotide is (i) a reference polynucleotide consisting of a sequence encoding the same mature polypeptide expressed by the Fab I gene contained in NCIMB Deposit No. 40771, or (ii) identical to the reference polynucleotide, except that over the entire length of the reference polynucleotide there are up to five amino acid substitutions, additions and deletions; or (b) the complement of the entire length of such first polynucleotide.

41. (Amended) A vector comprising the isolated polynucleotide of Claim 40, wherein the isolated polynucleotide is DNA.

42. A cultured host cell comprising the vector of Claim 41.

43. A process for producing a polypeptide comprising the step of expressing from the host cell of Claim 42 a polypeptide encoded by said DNA.

44. A process for producing a cell which expresses a polypeptide comprising transforming or transfecting the cell with the vector of Claim 41 such that the cell expresses the polypeptide encoded by the DNA contained in the vector.

45. A process for producing a Fab I polypeptide or fragment, which fragment retains binding and/or enzymatic activity, comprising culturing a host of claim 42 under conditions sufficient for the production of said polypeptide or fragment.

46. (Amended) An isolated polynucleotide comprising a DNA sequence obtained by screening a *Staphylococcus aureus* strain WCUH29 DNA library containing the complete gene encoding an amino acid sequence set forth in SEQ ID NO:2 under stringent hybridization conditions with a polynucleotide probe having a polynucleotide sequence set forth in SEQ ID NO:1 or a fragment thereof, which fragment is a 17-mer or longer, wherein stringent hybridization conditions means that hybridization will occur only if there is at least 95% identity between the sequences, where identity is determined using an algorithm consisting of BLASTN where the algorithm is adapted to give the largest match between sequences tested, over the entire length of the polynucleotide sequence or fragment thereof.

47. (Amended) The isolated polynucleotide of claim 1, which hybridizes under stringent conditions to a second reference polynucleotide consisting of the sequence of SEQ ID NO:1 or to the complement of the entire length of such second reference polynucleotide, wherein stringent conditions means that hybridization will occur only if there is at least 95% identity between the sequences, where identity is determined using an algorithm consisting of BLASTN where the algorithm is adapted to give the largest match between sequences tested, over the entire length of the second reference polynucleotide or the complement thereof.

48. (Amended) The isolated polynucleotide of claim 1, comprising (a) a first polynucleotide having at least 95% identity to the first reference polynucleotide, or (b) the complement of the entire length of such first polynucleotide.